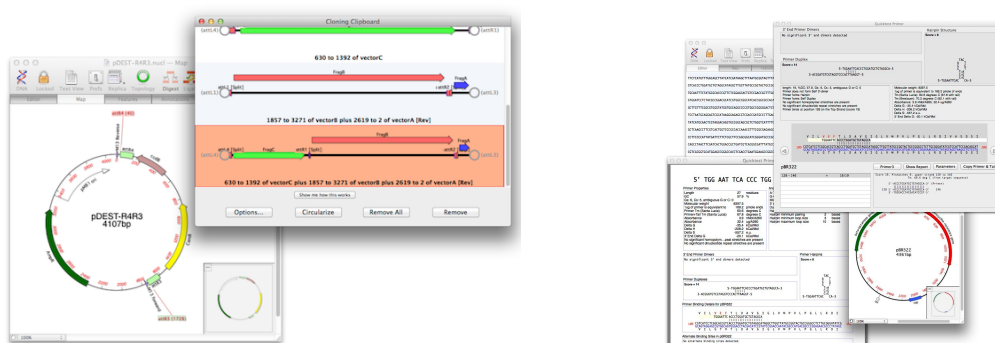


# MacVector

## WORKSHOPS

# You are invite to a MacVector 14 Workshop



**Wednesday, September 16 from 2pm to 4pm**

**at the UM Center for Environmental Sciences; 701 East Pratt St;  
Columbus Center 2038 (Multi Purpose Room)**

Dr. Kevin Kendall of MacVector, Inc. will be giving a workshop for both novice and advanced users of MacVector, reviewing both basic and advanced functions in MacVector. In particular, he will highlight the new functionality introduced over the last 2 years to MacVector. The format is very informal and participants are encouraged to ask questions and help direct the workshop towards areas of the most interest. We guarantee that everyone will learn at least one new thing about MacVector that will help your work.

To sign up for the workshop, please email Rosemary Maratta at [rmaratta@macvector.com](mailto:rmaratta@macvector.com).

## Course Title: MacVector 13.5 Training Workshop

**Description:** This is a training workshop designed to help both novice and advanced users of MacVector get the most out of the software.

### Objectives:

#### 1. Getting Started With MacVector

A basic overview targeted primarily at beginners, but also aims to make sure experienced users are aware of all the features and workflows offered by MacVector.

**Opening, importing and manipulating sequences**

**Basic sequence analysis functions.**

**Sequence alignments.**

**Sequence Assembly**

**Protein Analysis**

#### 2. Getting The Most Out Of MacVector

Functionality aimed at the slightly more experienced user.

How to use and configure MacVector to take advantage of the built-in workflows.

**Preferences** - what do all those functions do?

Adding and manipulating features, understanding GenBank features and files

**Auto-annotation** - using your existing files to annotate new sequences

**Quick sequence comparisons** - using the Pustell dot-plot analysis to quickly compare two sequences.

**Align To Reference** - SNPs, sequence confirmation and cDNA alignments

#### 3. New Features (MacVector 12 to 14)

A quick run through of the new functionality introduced over the last 2 years

Circular sequence support

The new graphics palette

Colors, case and translations in the Editor

One-out restriction enzyme sites and click-cloning enhancements

New multiple alignment algorithms

**NGS support**

Using **Bowtie** to map millions of reads to a reference genome

Using **Velvet** to create *de novo* assemblies

**Quicktest Primer** - intuitive interactive primer design taking structure, mismatches, translations and optional tails into account. Introduce mutations with a single click. view “one out” restriction sites.

Graphics performance - work with huge sequences graphically in real time

Directly paste data from copied GenBank/EMBL text data

Using the **Cloning Clipboard**

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